

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 11, 2003, 01:56:12 ; Search time 22 Seconds
(without alignments)
203.611 Million cell updates/sec

Title: US-09-914-324a-1
Perfect score: 616
Sequence: 1 MAAMADVDTPSGTNSGAGK.....KTRQVCPHLDNREMEFQKXGH 108

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209	33.9	84	AN11_MOUSE	Q9CPX9 mus musculus
2	208	33.8	84	AN11_HUMAN	Q9N9Y5 homo sapien
3	91	14.8	148	RN24_HUMAN	Q9Y225 homo sapien
4	90	14.6	600	RN12_MOUSE	Q9WLV7 mus musculus
5	88	14.3	161	Y0UD_CAEEL	P30631 caenorhabdi
6	87	14.1	624	RN12_HUMAN	Q9HW22 homo sapien
7	86	14.0	326	PEXA_HUMAN	O60683 homo sapien
8	83.5	13.6	115	YBR2_YEAST	P38239 saccharomyc
9	83	13.5	685	RNF6_HUMAN	Q9Y252 homo sapien
10	82.5	13.4	532	ICP0_HSVB	P28990 equine herp
11	80	13.0	284	GOLI_DROME	O06003 drosophila
12	79.5	12.9	796	PRH_AYATH	P48785 arabidopsis
13	79	12.8	381	RN13_CHICK	Q90972 gallus gall
14	79	12.8	381	RN13_HUMAN	O43567 homo sapien
15	79	12.8	410	ICP0_PVIF	P29129 pseudorabie
16	79	12.8	1680	FUR2_DROME	P30432 drosophila
17	78.5	12.7	235	Y057_CAEEL	O09463 caenorhabdi
18	78	12.7	381	RN13_MOUSE	O54965 mus musculus
19	77	12.5	279	SLI3_HUMAN	Q14192 homo sapien
20	77	12.5	295	PEXA_PICAN	O00940 picchia angu
21	76.5	12.4	758	YKDA_YEAST	P36096 saccharomyc
22	76	12.3	1493	M3K1_YEAST	P53349 mus musculus
23	76	12.3	1493	M3K1_RAT	O62825 rattus norv
24	76	12.3	1493	M3K1_HUMAN	O13333 homo sapien
25	75.5	12.3	676	ICP0_HSVB1	P29128 bovine herp
26	75.5	12.3	676	ICP0_HSVB2	P29838 bovine herp
27	74.5	12.1	825	ICP0_HSV2H	P28284 herpes simp
28	74	12.0	474	CBIC_HUMAN	O9U184 homo sapien
29	73.5	11.9	485	RNF8_HUMAN	O76064 homo sapien
30	73.5	11.9	488	RNF8_MOUSE	O8V556 mus musculus
31	72.5	11.8	416	YHR5_YEAST	P38823 saccharomyc
32	72.5	11.8	775	ICP0_HSV11	P08393 herpes simp
33	70.5	11.4	337	PEXA_YEAST	O05568 saccharomyc

34	70.5	11.4	342	ME18_MOUSE	P23798 mus musculus
35	70.5	11.4	344	ME18_HUMAN	P35227 homo sapien
36	70.5	11.4	467	ICP0_VZVD	O09309 varicella-z
37	70.5	11.4	585	YH80_YEAST	P38748 saccharomyc
38	70.5	11.4	610	Y0DA_CAEEL	O09268 caenorhabdi
39	70.5	11.4	1562	YMB1_YEAST	O04781 saccharomyc
40	70.5	11.4	2569	LM43_MOUSE	O61789 mus musculus
41	69.5	11.3	1238	Y009_CAEEL	O09298 caenorhabdi
42	69	11.2	353	REON_HUMAN	O92782 homo sapien
43	69	11.2	397	REON_MOUSE	P56163 rattus norv
44	69	11.2	507	MK3_HUMAN	O13064 homo sapien
45	69	11.2	564	YUES_CAEEL	P90859 caenorhabdi

ALIGNMENTS

RESULT 1	AN11_MOUSE	STANDARD:	PRT:	84 AA.
ID	AN11_MOUSE			
AC	Q9CPX9:			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Anaphase promoting complex subunit 11.			
GN	ANAPC11.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Embryo;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,			
RA	Kueth P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Kombaerts P.,			
RA	Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Williams L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,			
RA	Hayashizaki Y.,			
RT	"Functional annotation of a full-length mouse cDNA collection."			
RL	Nature 409:685-690(2001).			
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
CC	EMBL: AK003612; BAB22890.1; -			
CC	EMBL: AK003244; BAB22663.1; -			
CC	MGI: MGI:1913406; Anapc11.			
CC	InterPro: IPR001841; Znf_ring.			
CC	SMART: SM00184; RING_1.			
CC	PROSITE: PS00518; ZF_RING_1; FALSE_NEG.			
CC	PROSITE: PS50089; ZF_RING_2; 1.			
CC	Zinc-finger.			
FT	ZN_FING 34 77 RING-TYPE.			

DR EMBL: BC000213; AAH00213.1; -
 DR EMBL: AL079313; CAB45279.1; -
 DR HSSP: P28990; 1CHC.
 DR Genew: HGNC:13779; RNF24.
 DR InterPro: IPR001841; Znf_Ring.
 DR Pfam: PF00097; Zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR Zinc-finger.
 FT ZN_FING 78 119 RING-TYPE.
 FT CONFLICT 45 45 Y -> S (IN REF. 3).
 SQ SEQUENCE 148 AA; 17209 MW; 66C240C3A591EA5 CRC64;

Query Match 14.8%; Score 91; DB 1; Length 148;
 Best local Similarity 58.3%; Pred. No. 0.0032;
 Matches 14; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 75 CNAHFHCISRMLKTRQVCPDNR 98
 DB 96 CKHAFHRCIKLWLEVRKVCPLCN 119

RESULT 4
 RN12_MOUSE
 ID RN12_MOUSE STANDARD; PRT; 600 AA.
 AC 09WT7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE RING finger protein 12 (LIM domain interacting RING finger protein)
 DE (RING finger LIM domain-binding protein) (R-LIM).
 GN RNF12 OR RLIM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN 1)
 RP SEQUENCE FROM N.A.
 RA Bach I.;
 RT "Opposing developmental functions of positive and negative
 RT coregulators of LIM homeodomain factors."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN 2)
 RP FUNCTION.
 RX MEDLINE-99364422; PubMed-10431247;
 RA Bach I., Rodriguez-Esteban C., Carriere C., Bhushan A., Krone A.,
 RA Rose D.W., Glass C.K., Andersen B., Izpisua Belmonte J.C.,
 RA Rosenfeld M.G.;
 RT "LIM inhibits functional activity of LIM homeodomain transcription
 RT factors via recruitment of the histone deacetylase complex."
 RL Genet. 22:394-399(1999).
 CC -1- FUNCTION: ACTS AS A NEGATIVE CO-REGULATOR FOR LIM HOMEODOMAIN
 CC TRANSCRIPTION FACTORS. VIA THE RECRUITMENT OF THE SIN3A/HISTONE
 CC DEACETYLASE COREPRESSOR COMPLEX.
 CC -1- SUBUNIT: ASSOCIATES WITH LIM/HOMEOBOX FACTORS.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -----
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 CC -----
 DR EMBL: AF069992; AAD34209.1; -
 DR MGD: MGI:1342291; Rnf12.
 DR InterPro: IPR001841; Znf_Ring.
 DR Pfam: PF00097; Zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 DR PROSITE: PS50089; ZF_RING_2; 1.

KW Transcription regulation; zinc-finger.
 FT DOMAIN 415 484 SER-RICH.
 FT ZN_FING 546 587 RING-TYPE.
 FT DOMAIN 447 461 POLY-SER.
 SQ SEQUENCE 600 AA; 66470 MW; E68299530126EA1D CRC64;

Query Match 14.6%; Score 90; DB 1; Length 600;
 Best local Similarity 52.0%; Pred. No. 0.017;
 Matches 13; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 75 CNAHFHCISRMLKTRQVCPDNR 99
 DB 564 CSHEFHVCIDRMLSENSTPICRR 588

RESULT 5
 YOUND_CAEEL
 ID YOUND_CAEEL STANDARD; PRT; 161 AA.
 AC P30631;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical 18.8 kDa protein ZK637.14 in chromosome III.
 DE ZK637.14.
 GN ZK637.14.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN 1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RX MEDLINE-92168156; PubMed-1538779;
 RA Sulston J., Du Z., Thomas K., Wilson R., Hillier L., Staden R.,
 RA Halloran N., Green P., Thierry-Mieg J., Qiu L., Dear S., Coulson A.,
 RA Craxton M., Durbin R., Berks M., Metzstein M., Hawkins T.,
 RA Alnough R., Waterston R.,
 RT "The C. elegans genome sequencing project: a beginning."
 RL Nature 356:37-41(1992).
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -----

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 CC -----

DR EMBL: Z11115; CAA77447.1; -
 DR PIR: S15788; S15788.
 DR WormPep: ZK637.14; CE00432.
 DR InterPro: IPR001841; Znf_Ring.
 DR Pfam: PF00097; Zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS50089; ZF_RING_2; 1.
 KW Hypothetical protein; zinc-finger.
 FT ZN_FING 72 134 RING-TYPE.
 SQ SEQUENCE 161 AA; 18847 MW; F5BF9F3A839AC027 CRC64;

Query Match 14.3%; Score 88; DB 1; Length 161;
 Best local Similarity 31.1%; Pred. No. 0.0075;
 Matches 19; Conservative 12; Mismatches 22; Indels 8; Gaps 2;

QY 42 CAICRNHIM-----DLCICQANQASATSECTVAMGVCNNAHFHCISRMLKTRQVC 94
 DB 72 CAICDNLQNNVDIPEDHVIK-ELKIDPTTFGTIVMPCKHRHFHFCILWLDAQTC 130

QY 95 P 95
 DB 131 P 131

RESULT 6
 RN12_HUMAN STANDARD: PRT: 624 AA.
 ID RN12_HUMAN
 AC O9NMW2: Q9Y598;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE RING finger protein 12 (LIM domain interacting RING finger protein)
 GN RNF12 OR RLIM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20469411, PubMed=11013082;
 RA Ostendorff H.P., Bossenz M., Mincheva A., Copeland N.G., Gilbert D.J.,
 RA Jenkins N.A., Litcher P., Bach I.;
 RT "Functional characterization of the gene encoding RLIM, the
 RT corepressor of LIM homeodomain transcription factors.";
 RL Genomics 69:120-130(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Renal cell carcinoma;
 RX MEDLINE=99438124, PubMed=10508479,
 RA Scanlan M.J., Gordon J.D., Williamson B., Stockert E., Bander N.H.,
 RA Jorgensen V., Gure A.O., Jager D., Jager E., Knuth A., Chen Y.-T.,
 RA Old L.J.;
 RT "Antigens recognized by autologous antibody in patients with renal-
 RT cell carcinoma.";
 RL Int. J. Cancer 83:456-464(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Isegaki T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Magatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,
 RA Niimomiya K., Iwayanagi T.;
 RT "NDO human cDNA sequencing project.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ACTS AS A NEGATIVE CO-REGULATOR FOR LIM HOMEODOMAIN
 CC TRANSCRIPTION FACTORS. VIA THE RECRUITMENT OF THE SIN3A/HISTONE
 CC DEACETYLASE COREPRESSOR COMPLEX.
 CC -1- SUBUNIT: ASSOCIATES WITH LIM/HOMEOBOX FACTORS.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
 CC in position 134 and 142.
 CC -----
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 CC -----
 CC EMBL: AJ271670; CAC14228.1;
 DR EMBL: AF155109; AAD42875.1; ALT_FRAME.
 DR EMBL: AK001334; BAA91632.1;
 DR Genew: HGNC:13429; RNF12.
 DR MIM: 300379;
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4.1.
 DR SMART: SM00184; RING_1.
 DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE: PS00089; ZF_RING_2; 1.
 KW Transcription regulation; zinc-finger;
 FT DOMAIN 422 506 SER-RICH.
 FT ZN_FING 570 611 RING-TYPE.

FT DOMAIN 453 481 POLY-SER.
 FT DOMAIN 500 506 POLY-SER.
 FT CONFLICT 126 126 S -> C (IN REF. 1).
 FT CONFLICT 134 134 N -> D (IN REF. 3).
 FT CONFLICT 144 145 YS -> NR (IN REF. 3).
 FT CONFLICT 418 418 Y -> H (IN REF. 3).
 SO SEQUENCE 624 AA; 68527 MW; DE3ADE09ACACBCF8 CRC64;
 Query Match 14.1%; Score 87; DB 1; Length 624;
 Best Local Similarity 48.0%; Pred. No. 0.039;
 Matches 12; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
 OY 75 CNHAFPHCISRLKTRVCPIDNR 99
 Db 588 CSHEYVHCIDRWLSENSTPICRR 612
 ID PEXA_HUMAN STANDARD: PRT: 326 AA.
 AC O60683; Q9BM90;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Peroxisome assembly protein 10 (Peroxin-10).
 GN PEX10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT MALD GLN-290.
 RX MEDLINE=9834958; PubMed=9683594;
 RA Warren D.S., Morrell J.C., Moser H.W., Valle D., Gould S.J.;
 RT "Identification of PEX10, the gene defective in complementation
 RT group 7 of the peroxisome-biogenesis disorders.";
 RL Am. J. Hum. Genet. 63:347-359(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=98367027; PubMed=9700193;
 RA Okumoto K., Itoh R., Shimozawa N., Suzuki Y., Tamura S., Kondo N.,
 RA Fujiki Y.;
 RT "Mutations in PEX10 is the cause of Zellweger peroxisome deficiency
 RT syndrome of complementation group B.";
 RL Hum. Mol. Genet. 7:1399-1405(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain, and Lung;
 RA Strausberg R.;
 RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: SOMEWHAT IMPLICATED IN THE BIOGENESIS OF PEROXISOMES.
 CC -1- SUBCELLULAR LOCATION: PEROXISOMAL; MEMBRANE-ASSOCIATED
 CC (POTENTIAL).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; may be
 CC produced by alternative splicing.
 CC -1- DISEASE: DEFECTS IN PEX10 ARE THE CAUSE OF TWO FORMS OF ZELLWEGER
 CC SYNDROME; COMPLEMENTATION GROUP 7 (CG7) AND COMPLEMENTATION GROUP
 CC B (CGB). THESE ARE AUTOSOMAL RECESSIVE DISORDERS DUE TO DEFECTIVE
 CC IMPORT MECHANISMS FOR PEROXISOMAL MATRIX ENZYMES.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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 CC -----
 CC EMBL: AF060502; AAC18133.1;
 DR EMBL: AB013818; BAA87895.1;
 DR EMBL: BC000543; AAH00543.1;
 DR EMBL: BC018198; AAH18198.1;

DR HSP: P28990; ICHC.
 DR Genew; HGNC:8851; PEX10.
 DR MIM: 602859; -.
 DR MIM: 214100; -.
 DR InterPro; IPR001841; Znf_fing.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS00518; ZF_RING_1; 1.
 DR PROSITE; PS00089; ZF_RING_2; 1.
 KM Peroxisome; zinc-finger; Membrane; Disease mutation;
 KM Zellweger syndrome; Alternative splicing.
 FT ZN_RING 273 311
 FT VARSPLC 200 200
 FT VARIANT 290 290
 FT SEQUENCE 326 AA; 37069 MW; 9CF2CE5E4C797799 CRC64;
 SQ
 Query Match 14.0%; Score 86; DB 1; Length 326;
 Best Local Similarity 30.2%; Pred. No. 0.026;
 Matches 19; Conservative 11; Mismatches 23; Indels 10; Gaps 2;
 QY 43 AICRHHIMDLCEQANQASATSECTVAMGVCNHAFFHCISRWLKTQVCPDLDNREME 102
 DB 266 AVSRNPLCTLCLE-ERRHPTATP-----CGHLFCWECITAMCSSKAECPLCREKFP 315
 QY 103 FOK 105
 DB 316 FOK 318
 RESULT 8
 YBR2_YEAST
 ID YBR2_YEAST STANDARD; PRT; 115 AA.
 AC P38239;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 13.2 kDa protein in ORC2-TIP1 intergenic region.
 GN YBR062C OR YBR0528.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA Allinovic G., Pohl F.M., Pohl T.M.;
 RL Submitted (Aug-1994) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA Domdey H., Gassenhuber H., Obermaier B., Piravandi E.;
 RL Submitted (Aug-1994) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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 CC
 CC EMBL; Z35931; CAB85005.1; -
 DR PIR; S45920; S45920.
 DR SGD; S0000266; YBR062C.
 DR InterPro; IPR001841; Znf_fing.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS00089; ZF_RING_2; 1.
 KW Hypothetical protein; zinc-finger.

FT ZN_RING 44 88 RING-TYPE.
 SQ SEQUENCE 115 AA; 13241 MW; 745427AA3463DE71 CRC64;
 Query Match 13.6%; Score 83.5; DB 1; Length 115;
 Best Local Similarity 29.5%; Pred. No. 0.017;
 Matches 26; Conservative 6; Mismatches 25; Indels 31; Gaps 5;
 QY 17 AGKKREVKKNAVALMADIYVNDCAIC-RNHHM---LCIECQANQASATSECTVAM 72
 DB 28 ASLPRINKKKLKA-----TDNCSICTYNTLEDEYPLVLVLP------ 64
 QY 73 GVCNHAFFHCISRWLKTQVCPDLDN 98
 DB 65 --CHHKFDECTLSVWLSRSTTCPLCRDN 90
 RESULT 9
 RNFG_HUMAN
 ID RNFG_HUMAN STANDARD; PRT; 685 AA.
 AC Q9Y252; Q9YF41;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RING finger protein 6.
 GN RNFG.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE=99265977; PubMed=10331950;
 RA Macdonald D.H.C., Lahiri D., Sampath A., Chase A., Sohni J.,
 RA Cross N.C.P.;
 RT "Cloning and characterization of RNFG, a novel RING finger gene
 RT mapping to 13q12.";
 RL Genomics 58:94-97(1999).
 RN [2]
 RP SEQUENCE OF 320-685 FROM N.A.
 RC TISSUE=Testis;
 RA Blum H., Bauersachs S., Mewes H.-W., Gassenhuber J., Wiemann S.;
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- TISSUE SPECIFICITY: WEAKLY EXPRESSED IN PERIPHERAL BLOOD, SPLEEN,
 CC PROSTATE, TESTIS AND OVARY.
 CC
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 CC
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 CC
 CC EMBL; AJ010347; CAB40414.1; -
 DR EMBL; AJ010346; CAB40413.1; -
 DR EMBL; AL133621; CAB63747.1; -
 DR HSP; P28990; ICHC.
 DR Genew; HGNC:10069; RNFG.
 DR MIM; 604242; -
 DR InterPro; IPR001841; Znf_fing.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
 DR PROSITE; PS00089; ZF_RING_2; 1.
 KM ZINC-finger.
 FT ZINC_DOMAIN 292 424 ARG-RICH.
 FT DOMAIN 598 601 POLY-ASP.
 FT ZN_RING 632 673 RING-TYPE.
 SQ SEQUENCE 685 AA; 78091 MW; 34458477332E5EFC CRC64;
 Query Match 13.5%; Score 83; DB 1; Length 685;

OY 3 AAMDVDPSTGNSGAGKRRFEVKWNAVALMWDIVDNCALCRHINDLCECOANQAS 62
 DB 104 AAKMPTKTG-----KESDEK-----DLSDSCALC-----IE 131
 OY 63 ATSECTVAMGVCNNAHFHCISRLKTRQVCP 96
 DB 132 AYKPTDTRILPCCKHEFHKNCIDPMLIEHRCPM 165

RESULT 12
 PRH_ARATH STANDARD: PRT: 796 AA.
 AC P48785;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Pathogenesis-related homeodomain protein (PRHA).
 GN PRH OR PRHA OR AT4G2940 OR F27B13.180.
 OS Arabidopsis thaliana. (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=94312876; PubMed=7913642;
 RA Korfage U., Trezzini G.F., Meier I., Hahlbrock K., Somssich I.E.;
 RT "Plant homeodomain protein involved in transcriptional regulation of
 a pathogen defense-related gene.";
 RL Plant Cell 6:695-708(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98012533; PubMed=9351248;
 RA Plesch G., Stoereman K., Iovar Torres J., Walden R., Somssich I.E.;
 RT "Developmental and auxin-induced expression of the Arabidopsis prha
 homeobox gene.";
 RL Plant J. 12:635-647(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambolt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
 RA Harris B., Ansoorge W., Brandt P., Griwall L.A., Rieger M.,
 RA Welcheslgerter M., de Simone V., Obermaier B., Maché R., Meier M.,
 RA Kreis M., Delseny M., Pulgomech P., Watson M., Schmidheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohnsels J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Biham L., Robben J.,
 RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandennusche F.,
 RA Breken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weltzenegger T., Bothe G., Ransperger U., Hilbert H., Braun M.,
 RA Holzner E., Brandt A., Peters S., van Slaveren M., Dirks W.,
 RA Moolijman P., Klein Lankhorst R., Rose M., Hauf J., Koeller P.,
 RA Bernerster S., Hempel S., Feldpausch M., Lambers S., Van den Daale H.,
 RA De Keyser A., Buysnaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark U., Doggett J., Hall S., Kay M., Lennard N., Mcay K., Mayes R.,
 RA Petelt A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Borikova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fattmann B., Grandrath K., Dauner D., Herzl A.,
 RA Neumann S., Argitau A., Vitale D., Liguori R., Piravandi E.,
 RA Massenet O., Quigley F., Clabaud G., Mwendile A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chetoui F., Cooke R., Berger C., Montfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Baquies M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielek C.,
 RA Frisman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,

RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegler L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stokking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antonoli B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
 RA Granat S., Shohdy N., Hasegawa A., Hamed A., Lodi M., Johnson A.,
 RA Chen E., Maria M., Martensen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana";
 RL Nature 402:769-777(1999).
 CC -I- FUNCTION: SPECIFICALLY BINDS TO THE FUNGAL ELICITOR-RESPONSIVE
 DNA ELEMENT, 5'-CTATTGTTA-3', OF THE GENE PR2 PROMOTER.
 CC -I- SUBCELLULAR LOCATION: Nuclear.
 CC -I- INDUCTION: BY PATHOGEN INFECTION.
 CC -I- SIMILARITY: BELONGS TO THE PHD-ASSOCIATED HOMEBOX FAMILY.
 CC -I- SIMILARITY: CONTAINS 1 PHD-TYPE ZINC FINGER.
 CC -I- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.
 CC -----
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 CC -----
 DR EMBL: L21991; AAA3843.1; -;
 DR EMBL: U48864; AAC49836.1; -;
 DR EMBL: AL050352; CAB43668.1; -;
 DR EMBL: AL161575; CAB79752.1; -;
 DR TRANSFAC: T04108; -;
 DR InterPro: IPR001356; Homeobox.
 DR InterPro: IPR001965; Znf-PHD.
 DR Pfam: PF00046; homeobox.1.
 DR Pfam: PF00628; PHD.1.
 DR Pfam: P000010; Homeobox.1.
 DR SMART: SM00389; HOX.1.
 DR SMART: SM00249; PHD.1.
 DR PROSITE: PS50071; HOMEBOX_2; 1.
 DR PROSITE: PS01359; ZF-PHD_1; 1.
 DR PROSITE: PS50016; ZF-PHD_2; 1.
 KW Homeobox; DNA-binding; Nuclear protein; Transcription regulation;
 KW Repeat; Zinc-finger.
 FT ZN_FING 190 247
 FT DOMAIN 294 303 PHD-TYPE.
 FT DNA_BIND 452 511 ASP-RICH (ACIDIC).
 FT DOMAIN 605 735 HOMEBOX.
 FT REPEAT 605 631 5 X 27 AA TANDEM REPEATS.
 FT REPEAT 632 658 1.
 FT REPEAT 659 685 2.
 FT REPEAT 686 712 3.
 FT REPEAT 713 735 4.
 FT DOMAIN 738 759 5 (INCOMPLETE).
 FT LEUCINE-ZIPPER.
 SQ SEQUENCE 796 AA; 90657 MW; 5E61509A0CADB175 CRC64;

Query Match 12.9%; Score 79.5; DB 1; Length 796;
 Best Local Similarity 29.5%; Pred. No. 0.34;
 Matches 18; Conservative 12; Mismatches 26; Indels 3; Gaps 2;

OY 37 IVDNCAICRNHIMDCECOANQASATSECTVAMGVCNNAHFHCISRLKTRQVCP 96
 DB 179 VASDGSIHHDH--FCACNRSREA-FPNDIITLDCGTGNRAFHOKCLDPPIETESIPG 235
 OY 97 D 97
 DB 236 D 236

```
RESULT 13
RN13_CHICK STANDARD; PRT; 381 AA.
ID RN13_CHICK
AC 090972;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE RING finger protein 13 (C-RZF).
GN RNF13 OR RZF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
RC TISSUE=Brain;
RX MEDLINE=96181541; PubMed=8610176;
RA Tranque P., Crossin K.L., Cirelli C., Edelman G.M., Mauro V.P.;
RT "Identification and characterization of a RING zinc finger gene
(c-Rzf) expressed in chicken embryo cells."
RL Proc. Natl. Acad. Sci. U.S.A. 93:3105-3109(1996).
RN [2]
RP TISSUE SPECIFICITY
RA Lomax M.I., Warner S.J., Bersirli C.G., Gong T.-W.L.;
RT "The gene for a RING zinc finger protein is expressed in the inner
RT chick ear after noise exposure."
RL Prim. Sens. Neuron 2:305-316(1998).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Expressed primarily in brain and heart.
CC Also expressed in inner ear after noise exposure.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC
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DR EMBL: X95455; CA664725.1; -;
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR00137; PA.
DR InterPro: IPR001841; ZnF_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING_1.
DR SMART: SM00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Zinc-finger; Nuclear protein.
KW ZN_FING 240 282 RING-TYPE.
FT ZN_FING 240 282 RING-TYPE.
SQ SEQUENCE 381 AA; 42819 MW; 6816145C4033C6A CRC64;

Query Match 12.88; Score 79; DB 1; Length 381;
Best Local Similarity 29.38; Pred. No. 0.18;
Matches 17; Conservative 10; Mismatches 15; Indels 16; Gaps 3;

DB 40 DNCACRNMHMDLCIEQANQASATSECTVAMGVCMHAFHFCISRWL-KTRQVCP 96
238 DVCAICDEYED-----GDKRLRL-PCSHAYCKCVDPLTKTKTCV 280

RESULT 14
RN13_HUMAN STANDARD; PRT; 381 AA.
ID RN13_HUMAN
AC 043567;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE RING finger protein 13.
GN RNF13 OR RZF.

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lomax M.I., Warner S.J., Bersirli C.G., Gong T.-W.L.;
RT "The gene for a RING zinc finger protein is expressed in the inner
RT chick ear after noise exposure."
RL Prim. Sens. Neuron 2:305-316(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Yu W., Gibbs R.A.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and urinary bladder;
RX Strausberg R.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC
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DR EMBL: AF037204; AAC03769.1; -;
DR EMBL: AF070558; AAC28641.1; -;
DR EMBL: BC009803; AAH09803.1; -;
DR EMBL: BC009781; AAH09781.1; -;
DR Genbank: HGNC:10057; RNF13.
DR InterPro: IPR00137; PA.
DR InterPro: IPR001841; ZnF_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING_1.
DR SMART: SM00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR Zinc-finger; Nuclear protein.
KW ZN_FING 240 282 RING-TYPE.
FT ZN_FING 240 282 RING-TYPE.
SQ SEQUENCE 381 AA; 42813 MW; 4600727D0F197653 CRC64;

Query Match 12.88; Score 79; DB 1; Length 381;
Best Local Similarity 29.38; Pred. No. 0.18;
Matches 17; Conservative 10; Mismatches 15; Indels 16; Gaps 3;

DB 40 DNCACRNMHMDLCIEQANQASATSECTVAMGVCMHAFHFCISRWL-KTRQVCP 96
238 DVCAICDEYED-----GDKRLRL-PCSHAYCKCVDPLTKTKTCV 280

RESULT 15
ICP0_PRIVIF STANDARD; PRT; 410 AA.
ID ICP0_PRIVIF
AC P29129;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Trans-acting transcriptional protein ICP0 (Early protein 0) (EP0).
GN EP0.
OS Pseudorabies virus (strain Indiana-Purkhauer / Becker) (PRV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviridae;
OX NCBI_TaxID=31523;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374576; PubMed=1654441;
RA Cheung A.K.;


```

RT "Cloning of the latency gene and the early protein 0 gene of
RT pseudorabies virus."
RL J. Virol. 65:5260-5271(1991).
CC -!- FUNCTION: MAY BE A GENERAL TRANSACTIVATOR WHICH FUNCTIONS
CC SYNERGISTICALLY WITH IE180. IT MAY PLAY A ROLE IN THE REACTIVATION
CC OF LATENT PRV.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -!- SIMILARITY: TO OTHER HERPESVIRUSES ICPO PROTEIN.
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CC -----
DR EMBL: M57504; AAA47463.1; -.
DR HSSP: P28990; ICHC.
DR InterPro: IPR001841; znf_fing.
DR Pfam: PF00097; zf-CHC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
KW Transcription regulation; Trans-acting factor; Activator; Zinc-finger;
KW DNA-binding; Early protein.
FT ZN_FING 46 85
SQ SEQUENCE 410 AA; 43838 MW; E35384FE86F82D11 CRC64;

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Query Match 12.8%; Score 79; DB 1; Length 410;
Best Local Similarity 21.7%; Pred. No. 0.19;
Matches 18; Conservative 5; Mismatches 20; Indels 40; Gaps 1;

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OY 56 COANQASATSECTVAMGV-----C 75
DB 3 CTVSRRTTTAEKSSAMGIFGFRPSPSPQRLSLPTVMDCPICLDVAATEAQTLP 62
OY 76 NHAHFHCISRWLKTROVCPLDN 98
DB 63 MHHFCLDCIORWTLTSTACPLCN 85

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Search completed: May 11, 2003, 02:10:04
Job time : 25 secs

